FIGURE

12 3 6

```
n
              TPLGPRHPEPVEGRLASEUFPGEXANDGERANTUTAPPGYRLALYFTHFOLELSHLGTFDFVKLSSGARVLATLCDGESTOTERAF
     MASP-1
 1
                 NTVELHONFCQIQSPCYPDEYFSDEEVTHNETVPDGFRIKLYF WIFNLESSYLCEYDYVRVETEDQVLATFGGRETTDTRQTFGGEV 67
    MASP-1
                 CIBIPOKLIGEVISPLEPREPERPERPETTY (TYPTGYRVKLVF) QFDLEPSECGFYDYVKI SADRKSLGRFCCGLGSPLGHPPGKKE + 17
     cle
                     EPTHYGEILEPHEPQAYPSEVERENDIZVPEGYGIHLTF THLDIELSENÇAYDEVQIISGOTERGECGGRESHHPHEPLVE
    C13
                                                  . .
                                                          . .
L
                                         ETGERAFYAAEDIDECO VARGEA PTODHKOMHILGGFYGSGRACYVEHRKKATÇAALGE 170
              FYSLESSLOITFREDYSNERP
ū
     MASP-2
     HASP-L
              VLEPGSFHEITFREDFENSER
                                         PTGFDANYHAVDVDECK EREDEE LSCONYCHHYLOGYYCSCRPGYZLHTDHRTCRVEGS 167
177
              Pregonicilitentop sneergiinp y noplogaerix regeed popogomich my vogy poedrae goares
                                                                                                             177
                                      FTGFAAYYVATDINEET DEVO
                                                                      ANGERECHIE COCALCEES EALTHOOMSICCANCE
               POVPYNKLOVIFKEDFENSER
     CLE
              MASP+2
     MASP-1
              ONLFTGRTGVITSPOFPHPYPKSEECLYTIELEEGFMVHLOFE DIFDIED HPEVPCFFDYIELKVGPKVLGPFGGERAPEP 15TGS 253
m
              SELTTEASCYLESLEYPRSYPPOLECHYSTRVERGLTLHLEFL EFFDIDD HOCKHCPYDGLQ1YANGHIGEFCHHRHPD LDTSS 261
     Cle
              COUPTALIGETASPHYPKPYPE-TARGEYOLALEKGFGVVVTLAREEFEVKAADEACHG LOSLVFVADDROFGPVCHGFFGFLHTETKS 250
     Cla
               CCP-1 — CCP-1 — CCP-1 — MTVT:TFVTDESGDHTGWKIMYTSTAGPGFYPMAPPH GHVSPVQPKYILKDEFSIFQETGYELLGGHLPLKSFTAVCQADGEWDRPHPA
     MASP- I
              MSYLTLEPHSDMSGEMRGMRLSTRAAGMECPELOPPYM GKIEPSQPKYFFKDQVLVSGDTGYKVLKDMVEMOTPGIECIADGTWSMKIFF 342
NAVDLLPYTDESGLSRDMKLATTEIIKCPGPKILDEFTIIGNLGFJYGPRDYFIATCKGGYGLIECHGYLMSFTAVGGDGTMRAMPM 353
     HASP-1
     Clf
               NALOIIFGTOLTGGRRGWKLRYHGGPMPCPKEGTFN SVMEPAKAKYVPROVVGITCLOGPEVVRGRYGATSFYSTEGENGKNSNSKLK 3338
     C13
                   . . . . . .
              CSIVDGEPPDDLPSGHARAITGEDALLIANATGARGEELLALH
                                                                  KVNDGKYVCHADGFWTSEKGEKELPVCFVOCLS ARTT
     MASP-2
              CKIVOCRAPGELENGLITFSTRUNLTTYKEEIKYEGGEPYYKML
                                                                  NANTGIYTESACCVWWWKVLCHSLPTELPVCGLPRFSHKL
                                                                                                              126
     L-ERAP
               CKIKDCOOPENLPHGDFRYTTTMGVHTYKARIQYYCHEPYYXHGTE AUSRESEGGVYTCTAQGIHKNEGEGEKIPRCLEVGEKPVHPVEQ
     Clr
                                                                                                               443
              COPYDEGIPESIENGEVE OPESTLEGSVIRYTCEEPYTYME
                                                                  HGGGGEYHÇAGHGEWVHEVLGPELPKEVFVÇGVPREFFEE
     Cla
              GRIYGGGAARPGDFPWQVLILGGTTA AGALLYDNWVLTAAN
     MASP - 2
                                                                   AVYEORHDASALDIRMGTLERLSPHYTORWSEAVFIHED
                                                                                                               507
               MARIFMORPAQXOTTPWIAMLSHLMQQFFCGGSLLGSSWIVTAAHCLHQSLDFXDFTLRDSDLLEFSD FRIILGKKWRLRSDENEGHLG
     MASP-1
               RORIIGGGKAIDIGHFPHQVFTNIHGRG SGALLGDRWILTAAH
                                                                   TLYPKENEAGENACIOVELGNEVERIMELGNUP IRRV
                                                                                                               523
               KORIIGGSDADIKNFPHOVFFDHPHA GGALIHEYWYLTAAH
                                                                   VVEGNREPTHYVGSTSVQTSRLAKSRHLT PEHVFIHPG
                             o
fundialiklmnkvvinaniipiclprkeaesfratodigtasgrgutgrgflannlryvdipivdrgkctaayek
     MASP-1
              VKRTTLKPKYDPKTFEHOVALVELLEEPVLNAFVMPICLP
SVRPDYKODSSYN FEEDIALLELEESVTLGFNLLPICLP
DKDTFYDLGLAGYVSOFGYMEEK I ANDLRFYRLPVANPQACEN WLA
     MASP-1
                                                                                                               60 B
               WKLLEY PEGRTM FONDIALYRLKOPYKMGPTYSPICLPGTSSOYYLMDCDLGLISGMGRTEKEDRAVRLKAARLPYAHLRKCKEVKVE
     Clu
              PPYPRG SYTANMICAGLESGOKDSCRGDSGGALVFLDS ETER4FVGGIVSHGSHNEGRAGGYGVYTKVINYIPHIENIISDF
                                                                                                               671
     945P - 2
                        KYTROMECACEKEGGKDAGSGDSGGPMVTLNR ERGC MEVUTVSHOD DGGKKDRYGVYSYENONKOMIORVTGVRN
              APLKK
     MAS 2-1
               CANARIO VESCHIERDACOGOSGGVEAVROP NTDR WATGIVSHGI GESRG VGFYTKVLNYVDHIKKENEEED 688
KPTADALAYVETPHHIGAGGEK GROSGKGOSGGFAVGOPHOKTRFYAAGLVSHGP OCGT VGLYTRVONYVDHINKTHGENSTPRED 673
     cle
     013
                                        . . . . . . . . . .
                                                                 . . . . .
```

FIGURE

2

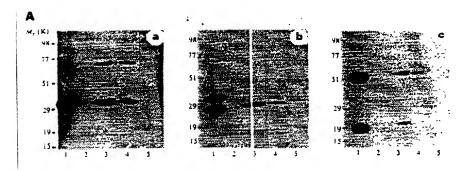


FIGURE 3A

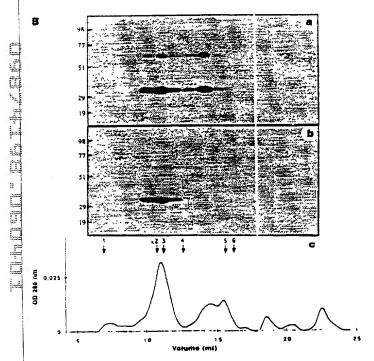


FIGURE 36

Ha&b

Classical pathway

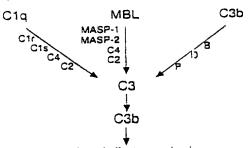
MS Lectin pathway

Alternative pathway

Antigen-antibody complexes

Microbial surfaces

Microbial surfaces



Activation of effector mechanisms

FIGURE

ctcgtgcaattcggcacgaggctggacgggcacaccATGAGGCTGCTGACCCTCCTGGGCCTTCTGTGTGGCTCGGTGGCCACCCCCTTAGGCCCGAAGT MRLLTLGLLCGSVAT 2 GGCCTGAACCTGTGTTCGGGCGCCCTGGCATCCCCCGGCTTTCCAGGGGAGTATGCCAATGACQAGGAGCGGCGCTGGACCCTGACTGCACCCCCCGGCTA 200 FGRLASPGFPGEYANDOERRW CCGCCTGCGCCTCTACTTCACCCACTTCGACCTGGAGCTCTCCCACCTCTGCGAGTACGACTTCGTCAAGCTCGGGGGCCCAAGGTGCTGCCACG 300 CTGTGCCGGCAGGAGACACAGACACGGAGCGGGCCCCTGGCAAGGACACTTTCTACTCGCTGGGCTCC? GCCTGGACATTACCTTCCGCTCCGACTACT 400 GKD Y S ERAP T F R S 106 ccaacgagaagccgttcacggggttcgaggccttctatgcagccgaggacattgacgagtgccaggtggi:cccgggagaggcgcccccacctgcgaccacca 500 Ε GCCACAACCACCTGGGCGGTTTCTACTGCTCCTGCCGGGAGGTACGTCCTGCACCGTAACAAGCG(ACCTGCTCAGCCCTGTGCTCCGGCCAGGTC 600 Ţc. ниньсск CRAG C S VLHRNKRTC TCACCCAGAGGTCTGGGGAGCTCAGCAGCCCTGAATACCCACGGCCGTATCCCAAACTCTCCAGTTGC//CTTACAGCATCAGCCTGGAGGAGGGGTTCA 700 800 ESFDVETHPETLCPYD: TGGCCCATTCTGTGGGAAGACATTGCCCCACAGGATTGAAACAAAAGCAACACGTGACCATCACCTT1GTCACAGATGAATCAGGAGACCACACACACGC 900 LPHRI TBOAAGATCCACTACACGAGCACAGCGCAGCCTTGCCCTTATCCGATGGCGCCCACCTATATGGCCACGTTTCACCTGTGCAAGCCAAATACATCCTGAAAG TAQP C P P ACAGCTTCTCCATCTTTTGCGAGACTGGCTATGAGCTTCTGCAAGGTCACTTGCCCCTGAAATCCTTTACTGCAGTTTGTCAGAAAGATGGATCTTGGGA 1100 ini "CCGGCCAATGCCCGCGTGCAGCATTGTTGACTGTGGCCCTCCTGATGATCTACCCAGTGGCCGAGTGGAGTACATCACAGGTCCTGGAGTGACCACCTAC 1200 PDDLPSGR<u>VEYITGPGVTT</u> CGP AAGCTGTGA'ITCAGTACAGCKGTGAAGAGACCTTCTACACAATGAAAGTGAATGATGGTAAATATGTCTGTGAGGGTGATGGTTCTGGACGAGCTCCA 1300 K A V I Q Y S C E E T F Y T M K V N D G K <u>Y V C E A D G F</u> W T S S AAGGAGAAAAATCACTCCCAGTCTGTGAGCCTGTTTGTGGACTATCAGCCCGCACAACAGGAGGGCGTFTATATGGAGGGAAAAAGGCAAAAACCTGGTGA 1400 CGLSARTTGGRIYGGQKAKP TTTTCCTTGGCAAGTCCTGATATTAGGTGGAACCACAGCAGCAGGTGCACTTTTATATGACAACTGGGTCCTAACAGCTGCTCATGCCGTCTATGAGCAA 1500 TAAGALLYDNW'LTAA HA A VYEQ WOVLILGGT 473 AAACATGATGCATCCGCCCTGGACATTTGGACTGCCCCTGAAAAGACTATCACCTCATTATACACA1.GCCTGGTCTGAAGCTGTTTTTATACATGAAG 1600 K H D A S A L D I R M G T L K R L S P H Y T Q A W S E A V F I H E 506 GTTATACTCATGATGCTGGCTTTGACAATGACATAGCACTGATTAAATTGAATAACAAAGTTGTAATCLATAGCAACATCACGCCTATTTGTCTGCCAAG 1,700 GŶTRDAGFDN<mark>M</mark>IALIKLNNKVVINSNITPICLP 1800 anagaagctgaatcctttatgaggacagatgacattggaactgcatctggatggggattaacccaaa/gggttttcttgctagaaatctaatgtatgtc K E A E S F M R T D D I G T A S G W G L T Q R G F L A R N L M Y 1900 GACATACCGATTGTTGACCATCAAAAATGTACTGCTGCATATGAAAAGCCACCCTATCCAAGGGGAAG GTAACTGCTAACATGCTTTGTGCTGGCTTAG DIPIVDHQKCTAAYEKPPYPRGSVTANMLCAGL 606 2000 aaagtggggcaaggacagctgcagaggtgacagggggcactggtgtttttagatagtgaaaca;aaaggtggtttgtgggaggaatagtgtcttg ESGGKDSCRGD^{est}GGALVFLDSETERWFVGGIV**SW** 640 gggttccatgaattgtggggaagcaggtcagtatggagtctacacaaaagttattaactatattccct;gatcgagaacataattagtgatitttaaell 2100 S M N C G E A G Q Y G V Y T K V I N Y I P & I E N I I S D Fatop 671 qeqtqtetqeagteaaggaltetteattittagaaatgeetg<mark>tgaaga</mark>oettggeagegaegtggetejagaageatteateateattactgtggaeatggea gttgttgctccacccaaaaaacagactccaggtgaggctgctgtcatttctccacttgccagtttaattccagccttacccattgactcaaggggacat 2300 aaacoacgagagtgacagtcatctttgcccacccagtgtaatgtcactgctcaaattacatttcattaccttaaaaagccagtctcttttcatactggct 2400

